

gi|12311218|emb|CAC22595.1| unnamed protein product [Hirudinaria manillensis]
Length = 488

Score = 962 bits (2486), Expect = 0.0
Identities = 488/488 (100%), Positives = 488/488 (100%)

Query: 1 KEIAVTIDDKNVIASVSESFHGVAFDASLSPKGWPSFVNITSPLKFLKLLLEGGLSPGYFRV 60
KEIAVTIDDKNVIASVSESFHGVAFDASLSPKGWPSFVNITSPLKFLKLLLEGGLSPGYFRV
Sbjct: 1 KEIAVTIDDKNVIASVSESFHGVAFDASLSPKGWPSFVNITSPLKFLKLLLEGGLSPGYFRV 60

Query: 61 GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFDDLVKLTG 120
GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFDDLVKLTG
Sbjct: 61 GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFDDLVKLTG 120

Query: 121 SKMRLLFDLNAEVRTGYEIGKTTSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS 180
SKMRLLFDLNAEVRTGYEIGKTTSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS
Sbjct: 121 SKMRLLFDLNAEVRTGYEIGKTTSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS 180

Query: 181 AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL 240
AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL
Sbjct: 181 AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL 240

Query: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGKTD 300
HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGKTD
Sbjct: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGKTD 300

Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360
VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV
Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360

Query: 361 GNTVFKVDVGDPTNKTRVYAQCTKTN SKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420
GNTVFKVDVGDPTNKTRVYAQCTKTN SKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG
Sbjct: 361 GNTVFKVDVGDPTNKTRVYAQCTKTN SKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420

Query: 421 KKIYSILTPEGQLTSQVVLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD 480
KKIYSILTPEGQLTSQVVLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD
Sbjct: 421 KKIYSILTPEGQLTSQVVLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD 480

Query: 481 ANVEACKK 488
ANVEACKK
Sbjct: 481 ANVEACKK 488

>gi|12311214|emb|CAC22593.1| unnamed protein product [Hirudinaria manillensis]
Length = 488

Score = 905 bits (2340), Expect = 0.0
Identities = 463/488 (94%), Positives = 471/488 (96%)

Query: 1 KEIAVTIDDKNVIASVSESFHGVAFDASLSPKGWPSFVNITSPLKFLKLLLEGGLSPGYFRV 60
KEIAVTIDDKNVIAS S SF GVAFDASLSPKG WSFV+ITSPKFLKLLLEGGLSPGYFRV
Sbjct: 1 KEIAVTIDDKNVIASASGSFLGVAFDASLSPKGWPSFVNITSPLKFLKLLLEGGLSPGYFRV 60

Query: 61 GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFDDLVKLTG 120
GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFD+LVKLTG
Sbjct: 61 GGTGANWLFFDLDENNWKDYWAFKDCKTPETATITRRWLFRKQNNLKETFDNLVLTG 120

Query: 121 SKMRLLFDLNAEVRTGYEIGKTTSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS 180
SKMRLLFDLNAEVRTGYEIGKK TSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS
Sbjct: 121 SKMRLLFDLNAEVRTGYEIGKMTSTWDSSAEKLFKYCVSKGVDNIDWELGNEPDHTS 180

Query: 181 AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL 240
AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL
Sbjct: 181 AHNLTEKVQVGEDFKALHKVLEKYPTLNKGSPVGPVGMGVSYVKGLADGAGDLVTAFTL 240

Query: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGKTD 300
HQYYFDGNTSDVS YLDA+YFKKLQQLFDKVKDVLK+SPHKD+PLWLGETSSG NSGT+D
Sbjct: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSTED 300.

Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360
VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV
Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360
Query: 361 GNTVFVVDVGDPTNKTRVYAQCTKTN SKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420
GNTVFVVDV DPTNK RVYAQCTKTN SKHTQ +YYKGSLTIFALNVGD +VTLKI QY G
Sbjct: 361 GNTVFVVDVSDPTNKARVYAQCTKTN SKHTQS RYYKGSLTIFALNVGDVTLKIGQQYSG 420
Query: 421 KKIYSIILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTGFVVSD 480
KKIYSIILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTGFVVSD
Sbjct: 421 KKIYSIILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTGFVVSD 480
Query: 481 ANVEACKK 488
ANVEACKK
Sbjct: 481 ANVEACKK 488

[>gi|12311216|emb|CAC22594.1| unnamed protein product [Hirudinaria manillensis]
Length = 488

Score = 904 bits (2337), Expect = 0.0
Identities = 462/488 (94%), Positives = 471/488 (96%)

Query: 1 KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGWSFVNITS PKLFLKLLLEG LSPGYFRV 60
KEIAVTIDDKNVIAS SESFHGVAFDASLFSPKG WSFV+ITSPKLFKLLLEG LSPGYFRV
Sbjct: 1 KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGWSFV DITS PKLFLKLLLEG LSPGYFRV 60
Query: 61 GGTFA NWLFFDLDENNWKD YWAFKD KTPETATITRRLFLRKQNNLK KETFDDLVLKLT KG 120
GGTFAN LFFDLDENNWKD YWAFKD KTPETATITRRLFLRKQNNLK KETFD+LVKLT KG
Sbjct: 61 GGTFA NWLFFDLDENNWKD YWAFKD KTPETATITRRLFLRKQNNLK KETFDNLV KLT KG 120
Query: 121 SKMRLLF DLNAEV RTGYEIGKTTSTWDS SSEA EKLFK YCVSKG YGD NIDWE LGNE PDHTS 180
SKMRLLF DLNAEV RTGYEIGK K TSW DSSSEA EKLFK YCVSKG YGD NIDWE LGN PDHTS
Sbjct: 121 SKMRLLF DLNAEV RTGYEIGK KMTSTWDS SSEA EKLFK YCVSKG YGD NIDWE LGNGPDHTS 180
Query: 181 AHNLT EKQVGED FKF ALHKV LEKY PTLN KGS PVGP DVGMGV SYVK GLAD GAGD LVTA FTL 240
AHNLTEKQVGED FKF ALHKV LEKY PTLN KGS VGP DVGMGV SYVK GLAD AGD VTA FTL
Sbjct: 181 AHNLT EKQVGED FKF ALHKV LEKY PTLN KGS LVGP DVGMGV SYVK GLADE AGDH VTA FTL 240
Query: 241 HQYYFDGNT SDV STYLD ASYFKKLQQLFDKVKDV LKN SPHKDKPLWL GETSSGC NSGT KD 300
HQYYFDGNT SDVS YLDA+YFKKLQQLFDKVKDV LK+SPHKDKPLWL GETSSG NSGT+D
Sbjct: 241 HQYYFDGNT SDV SIYLD ATYFKKLQQLFDKVKDV LKDSPHKDKPLWL GETSSG NSGT ED 300
Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360
VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIY+GYG LDKNTLEPNPDYWLMHVHNSLV
Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYSGYYGPLDKNTLEPNPDYWLMHVHNSLV 360
Query: 361 GNTVFVVDVGDPTNKTRVYAQCTKTN SKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420
GNTVFVVDV DPTNK RVYAQCTKTN SKHTQ +YYKGSLTIFALNVGD +VTLKI QY G
Sbjct: 361 GNTVFVVDVSDPTNKARVYAQCTKTN SKHTQS RYYKGSLTIFALNVGDVTLKIGQQYSG 420
Query: 421 KKIYSIILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTGFVVSD 480
KKIYSIILTPEGGQLTSQKVLLNGKELNL SDQLP+LNADESKTSFTLSPKTGFVVSD
Sbjct: 421 KKIYSIILTPEGGQLTSQKVLLNGKELNLXSDQLPQLNADESKTSFTLSPKTGFVVSD 480
Query: 481 ANVEACKK 488
ANVEACKK
Sbjct: 481 ANVEACKK 488